REMARKS

The specification, sequence listing and claims 1, 4, 12, 22, 24, 25, 34, 35, 44, 45, 46, 47, 48, 52, 53, 54, and 56 have been amended to include recitation of new nucleotide sequences SEQ ID NO:35 and 37 and amino acid sequences SEQ ID NO:36 and 38.

New matter has been added by this amendment, prior to the expiration of the priority year (Aug. 1, 2001).

The amendments are designated above and below using underlining where the text has been added.

For the convenience of the examiner, a substitute specification, a marked-up copy of the original specification, and substitute sequence listing are submitted herewith.

No fee is believed due with this amendment. If any fees are required, please charge them to the Deposit Account No. 50-1744 (in the name of Syngenta).

Respectfully submitted,

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Date: July 20, 2001

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Version of Specification and Claims Showing Amendments

IN THE SPECIFICATION:

Please amend the specification to read as follows:

On page 3, second paragraph:

-- In one aspect, the present invention encompasses novel methods for controlling gene silencing in a plant cell. The present invention encompasses the suppression of gene silencing or the increase in gene silencing in plants. In a preferred embodiment, this is achieved by altering the expression in the plant cell of a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain. In another embodiment, the nucleotide molecule encodes a polypeptide comprising exonuclease activity, preferably having 3'-5' RNA exonuclease activity. Preferably, the polypeptide comprises a 3'-5' exonuclease domain. More preferably, the 3'-5' exonuclease domain is an RNase D related domain. In another preferred embodiment, the polypeptide is identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16 SEQ ID NO:18, SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38. Preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37. Most preferably, the nucleotide sequence is identical or substantially identical to SEQ ID NO:23.--

On page 3, fourth paragraph:

--In a preferred embodiment, the expression of a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain is altered by altering its transcription or translation. Reduced expression is for example obtained by expressing in the plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 in sense orientation, or a portion thereof; or expressing in the plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11 SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 in anti-sense orientation, or a portion thereof; or expressing in the plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:13, [or] SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:13, [or] SEQ ID NO:23,

SEQ ID NO:35 or SEQ ID NO:37 or a portion thereof, and an anti-sense RNA of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11 SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or modifying by homologous recombination in said plant cell at least one chromosomal copy of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEO ID NO:23, SEO ID NO:35 or SEO ID NO:37 or of a regulatory region thereof; or expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or to a regulatory region thereof; or introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a regulatory region thereof. Preferably, the expression of the sequence is altered by insertional mutagenesis, point mutation or deletion mutagenesis of the genomic copy of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEO ID NO:21, SEO ID NO:9, SEO ID NO:11, SEO ID NO:13, [or] SEO ID NO:23, SEO ID NO:35 or SEQ ID NO:37 or a regulatory region thereof. Alternatively, the sequence has a mutation due to rearrangement .--

On page 5, fourth paragraph:

--The present invention also encompasses an expression cassette comprising a nucleic acid molecule of the present invention comprising a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain, or complement thereof. Preferably, the expression cassette comprises a nucleic acid molecule comprises a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37.--

On page 6, third paragraph:

-- An isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain ,and wherein the polypeptide is identical or substantially similar to an amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38 or complements thereof. Preferably, the polypeptide is identical or substantially --

On page 7, first paragraph:

-- similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:22. More preferably, the polypeptide is identical or substantially similar to SEQ ID NO:2 or SEQ ID NO:24. In another preferred embodiment, the nucleotide sequence is identical or substantially similar to a nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37. Preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, or SEQ ID NO:23. More preferably, the nucleotide sequence is substantially similar to SEQ ID NO:1. Most preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:23. In another preferred embodiment, the 3'-5' exonuclease domain preferably comprises an RNase D related domain Preferably, the polypeptide comprises 3'-5' exonuclease activity, and most preferably, 3'-5' RNA exonuclease activity. In yet another preferred embodiment, the nucleotide sequence is derived from a plant.--

On page 7, second paragraph:

-- The present invention further provides an isolated recombinant nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide encoded by the amino acid sequence identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38, or complements thereof. More preferably, the recombinant nucleic acid molecules comprise the nucleotide sequence of SEQ ID NO:23 or complement thereof. The recombinant nucleic acid molecule is operatively linked to a promoter functional in a cell. Preferably, the promoter is functional in a plant cell. --

On page 7, third paragraph:

-- An isolated and substantially purified polypeptide comprising an amino acid sequence identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16 SEQ ID NO:18, [or] SEQ ID NO:24, SEQ ID NO:36, or SEQ ID NO:38. Preferably, the polypeptide comprises the amino acid sequence of SEQ ID NO:24. Alternatively, the polypeptide consists of the amino acid sequence of SEQ ID NO:24.--

On page 8, third paragraph:

-- A cell comprising the nucleic acid or recombinant nucleic acid molecule of the present invention, and a cell comprising the expression cassette of the present invention Preferably, the cell is a plant cell. In a preferred embodiment, the nucleotide sequence of the present invention is expressed in said plant cell. In another preferred embodiment, the expression cassette promoter is a constitutive promoter, an inducible promoter, a tissue-specific promoter or a developmentally-regulated promoter. In another preferred embodiment, the expression cassette or recombinant nucleic acid molecule is stably integrated in the genome of the plant cell. In yet another preferred embodiment, the plant cell comprises an endogenous nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37. Preferably, the endogenous nucleotide sequence is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 SEQ ID NO:21, or SEQ ID NO:23. More preferably, the endogenous nucleotide sequence is identical or substantially similar to SEQ ID NO:1. Most preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:23. Preferably, the expression of said endogenous nucleotide sequence in said plant cell is altered.--

On page 9, first paragraph:

-- A plant cell comprising an endogenous nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 and wherein said plant cell comprises a mutation in said endogenous nucleotide sequence, or in a regulatory region thereof. Preferably, said mutation is due to the insertion of a nucleic acid molecule into said endogenous nucleotide sequence or into a regulatory region thereof, wherein the expression of said endogenous nucleotide sequence in said plant is altered. Preferably, the endogenous--

On page 9, fifth paragraph:

-- A plant cell or plant capable of expressing a sense RNA molecule of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 and an anti-sense RNA molecule of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 wherein said sense and said anti-sense RNA molecules are capable of forming a double-stranded RNA molecule. An advantage of the invention is that the expression in said plant cell of an endogenous nucleotide sequence of said plant cell that is substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 is reduced.--

On page 10, third paragraph:

-- A method for altering the expression of an endogenous nucleotide sequence that is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 in a plant cell or plant comprising the step of: altering the transcription or translation of said endogenous nucleotide sequence in said plant cell or plant.

In a preferred embodiment, wherein altering the transcription or translation of said endogenous nucleotide sequence in said plant cell or plant comprises the step of:

- a) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a portion thereof, in sense orientation; or
- b) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a portion thereof, in anti-sense orientation; or

- c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or
- d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially --

On page 11, first paragraph:

- --similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; or
- e) modifying by homologous recombination in said plant cell at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or of a regulatory region thereof; or
- f) expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or to a regulatory region thereof; or
- g) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a regulatory region thereof.--

On page 11, second paragraph:

-- A method for altering the expression of an endogenous nucleotide sequence that is as described or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 in

a plant cell comprising introducing into said plant cell a means for altering the transcription or translation of said endogenous nucleotide sequence in said plant cell.--

On page 11, third paragraph:

- -- A method for altering the expression of a nucleotide sequence of interest in a plant cell or plant comprising the steps of:
- a) altering the expression in said plant cell or plant of an endogenous nucleotide sequence of said plant cell that is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; and
- b) introducing into said plant cell a nucleic acid molecule comprising said nucleotide sequence of interest, wherein the expression of said nucleotide sequence of interest in said plant cell or plant is altered.--

On page 12, first paragraph:

- -- a) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in sense orientation; or
- b) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in anti-sense orientation; or
- c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or

- d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or
- e) modifying by homologous recombination in said plant cell at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or of a regulatory region thereof; or
- f) expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13,[or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or to a regulatory region thereof; or
- g) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide identical or sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a regulatory region thereof.--

On page 13, first paragraph:

- -- A method for stabilizing the expression of a nucleotide sequence of interest in a plant cell comprising:
- a) altering the expression in a plant cell of an endogenous nucleotide sequence of said plant cell that encodes a polypeptide comprising a 3'-5' exonuclease domain, and wherein said polypeptide is identical or substantially similar to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, [or] SEQ ID NO:24, SEQ ID NO:36 and SEQ ID NO:38; and
 - b) introducing into said plant cell a nucleotide sequence of interest, --

On page 13, third paragraph through page 14:

-- Preferably, the polypeptide has 3'-5' RNA exonuclease activity. Preferably, the 3'-5' exonuclease domain is an RNase D related domain. Preferably, the endogenous nucleotide sequence is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5,

SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37.

Preferably, the expression of said endogenous nucleotide sequence is altered by:

- a) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in sense orientation; or
- b) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, <u>SEQ ID NO:35 or SEQ ID NO:37</u>, or a portion thereof, in anti-sense orientation; or
- c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or
- d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; or
- e) expressing in said plant cell an aptamer specifically directed to a polypeptide identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38; or
- f) modifying by homologous recombination in said plant cell at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID--On page 15, first partial paragraph:
- -- NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, <u>SEQ ID NO:35 or SEQ ID NO:37</u>, or of a regulatory region thereof; or

- g) expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or to a regulatory region thereof; or
- h) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, <u>SEQ ID NO:35 or SEQ ID NO:37</u>, or a regulatory region thereof.--

On page 15, first paragraph:

-- The present invention further provides:

A method for identifying a compound capable of interacting with a polypeptide comprising a 3'-5' exonuclease domain comprising:

- a) combining a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, [or] SEQ ID NO:24, <u>SEQ ID NO:36 or SEQ ID NO:38</u>, or a homolog thereof, and a compound to be tested for the ability to interact with said polypeptide, under conditions conducive to interaction; and
- b) selecting a compound from step (a) that is capable of interacting with said polypeptide.--

On page 15, second paragraph:

-- Preferably, the polypeptide is encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37.--

On page 16, amend the sequence listing to read as follows:

---- SEQ ID NO:9 nucleotide sequence corresponding to GenPept accession AAD26968

SEQ ID NO:10 GenPept accession AAD26968

SEQ ID NO:11 nucleotide sequence corresponding to GenPept accession AAC25931

SEQ ID NO:12 GenPept accession AAC25931

SEQ ID NO:13 nucleotide sequence corresponding to GenPept accession AAF98185

SEQ ID NO:14 GenPept accession AAF98185

- SEQ ID NO:15 nucleotide sequence corresponding to GenPept accession CAA80137
- SEQ ID NO:16 GenPept accession CAA80137
- SEQ ID NO:17 nucleotide sequence corresponding to GenPept accession AAF06162
- SEQ ID NO:18 GenPept accession AAF06162
- SEQ ID NO:19 Oligonucleotide 3' specific primer
- SEQ ID NO:20 Oligonucleotide pD991 primer
- SEQ ID NO:21 corrected nucleotide sequence corresponding to corrected GenPept accession AAC42241
- SEQ ID NO:22 corrected GenPept accession AAC42241
- SEQ ID NO:23 nucleotide sequence of cDNA encoding a polypeptide comprising a

RNase D related domain from Arabidopsis thaliana

- SEQ ID NO:24 amino acid sequence of polypeptide comprising a RNase D related domain from *Arabidopsis thaliana*
- SEQ ID NO:25 oligonucleotide T-DNA specific primer LB1
- SEQ ID NO:26 oligonucleotide T-DNA specific primer LB2
- SEQ ID NO:27 oligonucleotide T-DNA specific primer LB3
- SEQ ID NO:28 oligonucleotide arbitrary degenerate primer AD3
- SEQ ID NO:29 oligonucleotide primer 36851TD#3
- SEQ ID NO:30 gene-specific oligonucleotide primer L22F4F
- SEQ ID NO:31 gene-specific oligonucleotide primer F22L4R
- SEQ ID NO:32 oligonucleotide primer AtWRN CDS F
- SEQ ID NO:33 oligonucleotide primer AtWRN-RT-R
- SEQ ID NO:34 oligonucleotide primer AtWRN CDS R
- SEQ ID NO:35 nucleotide sequence corresponding to GenPept accession AAG50917
- SEQ ID NO:36 GenPept accession AAG50917
- SEQ ID NO:37 nucleotide sequence corresponding to GenPept accession BAB11227
- SEQ ID NO:38 GenPept accession BAB11227--

On page 23, first paragraph:

-- The inventors of the present invention are the first to screen for plant nucleotide sequences encoding a polypeptide comprising a 3'-5' exonuclease domain, and to successfully identify such nucleotide sequences. This is carried out according to the methods disclosed in Example 1. The amino acid sequences and corresponding nucleotide sequences identified using the method and algorithms disclosed in Example 1 are set forth in SEQ ID NO:1-14, and 35-38 and briefly

described as follows. An amino acid sequence predicted from a genomic sequence from Arabidopsis thaliana is found in GenBank under accession #CAB36851 and is set forth in SEQ ID NO:2. The corresponding nucleotide sequence is found in BAC F18A5, GenBank accession number AL035528.2. An amino acid sequence predicted from a genomic sequence from Arabidopsis thaliana is found in GenBank under accession #AAD25623 and is set forth in SEQ ID NO:4. The corresponding nucleotide sequence is found in BAC F20D21, GenBank accession number AC005287.4. An amino acid sequence predicted from a genomic sequence from Arabidopsis thaliana is found in GenBank under accession #AAC69936 and is set forth in SEQ ID NO:6. The corresponding nucleotide sequence is found in Arabidopsis thaliana chromosome II section 181 of 255, GenBank accession number AC005700.2. An amino acid sequence predicted from a genomic sequence from Arabidopsis thaliana is found in GenBank under accession #AAC42241 and is set forth in SEQ ID NO:8. The corresponding nucleotide sequence is found in Arabidopsis thaliana chromosome II section 145 of 255, GenBank accession number AC005395.2. An amino acid sequence predicted from a genomic sequence from Arabidopsis thaliana is found in GenBank under accession #AAD26968 and is set forth in SEQ ID NO:10. The corresponding nucleotide sequence is found in Arabidopsis thaliana chromosome II section 197 of 255, GenBank accession number AC007135.7. An amino acid sequence predicted from a genomic sequence from Arabidopsis thaliana is found in GenBank under accession #AAC25931 and is set forth in SEQ ID NO:12. The corresponding nucleotide sequence is found in Arabidopsis thaliana chromosome II section 182 of 255, GenBank accession number AC004681.2. An amino acid sequence predicted from a genomic sequence from Arabidopsis thaliana is found in GenBank under accession #AAF98185 and is set forth in SEQ ID NO:14. The corresponding nucleotide sequence is found in BAC F17F8, GenBank accession number AC000107.2. An amino acid sequence predicted from a genomic sequence from Arabidopsis thaliana is found in GenBank under accession # AAG50917 and is set forth in SEQ ID NO:36. The corresponding nucleotide sequence is found in BAC F14G9, GenBank accession number AC069159. An amino acid sequence predicted from a genomic sequence from Arabidopsis thaliana is found in GenBank under accession # BAB11227 and is set forth in SEQ ID NO:38. The corresponding nucleotide sequence is found in BAC K16H17, GenBank accession number AB016884.--

On page 24, second paragraph,

--Further, the present invention provides for nucleic acid molecules encoding a full length nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain of SEQ ID

NO:24 as was cloned from Arabidopsis thaliana as set forth in Examples 2-3. The invention also provides a nucleic acid molecule comprising or having the sequence identical or substantially similar to the nucleotide sequence of SEQ ID NO:23 or complements thereof. The inventors of the present invention predicted a 3'-5' exonuclease domain between about amino acid positions 129 and 287 in the amino acid sequence set forth in SEQ ID NO:2. The inventors of the present invention also predicted that the amino acid sequence between about amino acid positions 136 and 271 in SEQ ID NO:4 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 76 and 210 in SEQ ID NO:6 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 46 and 199 in SEQ ID NO:22 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 57 and 193 in SEQ ID NO:10 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 66 and 202 in SEQ ID NO:12 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 380 and 538 in SEQ ID NO:36 is comprised in a 3'-5' exonuclease domain, that the amino acid sequence between about amino acid positions 30 and 193 in SEQ ID NO:38 is comprised in a 3'-5' exonuclease domain. The inventors of the present invention also predict that the amino acid sequence between about amino acid positions 129 and 282 in SEQ ID NO:24 comprises a 3'-5' exonuclease domain. --

On page 24, fourth paragraph:

-- Thus, the present invention discloses a nucleotide sequence encoding a polypeptide identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, [or] SEQ ID NO:14, SEQ ID NO:36 or SEQ ID NO:38. Preferably, the polypeptide is identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, or SEQ ID NO:22. More preferably, the polypeptide is identical or substantially similar to SEQ ID NO:2. Most preferably, the polypeptide is identical or substantially similar to the amino acid sequence of SEQ ID NO:24.--

On page 24, fifth paragraph through page 25:

-- Preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11 SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37. More preferably, the nucleotide sequence is substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, or SEQ ID NO:21. Yet more preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:1.

Most preferably, the nucleotide sequence is identical or substantially similar to SEQ ID NO:23. --

On page 25, third paragraph:

-- Based on Applicants' disclosure of the present invention, nucleotide sequences encoding polypeptides identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38 are isolated, preferably from the genome of any desired plant. For example, all or part of the nucleotide sequence set forth in SEQ ID NO:1 is used as a probe that selectively hybridizes to other nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e. genomic or cDNA libraries) from a chosen source organism. Such techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, e.g. Sambrook et al., "Molecular Cloning", eds., Cold Spring Harbor Laboratory Press. (1989)) and amplification by PCR using oligonucleotide primers corresponding to sequence domains conserved among such polypeptides (see, e.g. Innis et al., "PCR Protocols, a Guide to Methods and Applications", Academic Press (1990)). For example, oligonucleotide primers corresponding to a portion of a 3'-5' exonuclease domain are used. These methods are particularly well suited to the isolation of nucleotide sequences from organisms closely related to the organism from which the probe sequence is derived. Isolation of such a nucleic acid molecule of the present invention, in particular SEQ ID NO:23, is described in Example 7. --

On page 44, third paragraph:

-- VIII. Polypeptides encoded by the nucleic acid molecules.

The present invention provides polypeptides encoded by the nucleic acid molecules of the invention and variants thereof. These polypeptides are exemplified by those encoded by the nucleotide sequences of SEQ ID NOS: 2, 4, 6, 22, 18, 12, 14, [and] 24, 36 and 38; polypeptides encoded by nucleic acid sequences having at least 70% sequence similarity to the sequences of SEQ ID NOS: 1, 3, 5, 21, 9, 11, 13, [or] 23, 35 or 37 and variants and mutants thereof. Preferably, the isolated and substantially purified polypeptides are identical or substantially similar to the amino acid sequence of SEQ ID NO:24.--

On page 47, first paragraph:

-- The 3'-5' exonuclease domain consists of three sequence motifs termed Exo I, Exo II, and Exo III (Moser et al. (1997) *Nucl. Acids Res.* 25:5110-5118). These motifs are clustered around the active site and contain four negatively charged amino acids that serve as ligands for the two metal

ions necessary for catalysis in addition to a catalytically active tyrosine. The presence of these amino acids in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, and SEQ ID NO:18, and their position in the corresponding amino acid sequences is indicated in Table 1 below. The positions of the exo I, exo II, and exo III motifs in these amino acid sequences is shown in Table 2.

Method 3

Additional Arabidopsis genes that encode proteins with 3'-5' exonuclease domains are identified starting from the experimentally determined cDNA sequence for the gene encoded by SEQ ID NO:1. This protein sequence (SEQ ID NO:24) is identified as described in Example 6 (see below). A BLASTp search (Altschul, S.F. et al. (1997) *Nucleic Acids Res.* 25:3389-3402) with SEQ ID NO:24 as the query reveals that there are several predicted Arabidopsis proteins with E values less than 1E-03. From this group of Arabidopsis proteins, a HMM search is performed with each protein as a query compared to the HMM database of PFAM models (version 6.4) on a TimeLogic DeCypher machine. Two Arabidopsis proteins (AAG50917 (SEQ ID NO:36) and BAB11227 (SEQ ID NO:38)) are identified that were not identified by methods 1 and 2 earlier. The nucleotide sequences corresponding to AAG50917 and BAB11227 are SEQ ID NO:35 and SEQ ID NO:37, respectively. These proteins have E values from the HMM search that are below 1E-01 and likely to be significant. For comparison, the E-values for all the Arabidopsis proteins identified in Example 1 are shown in the third column in Tables 1 and 2 as recalculated with the same HMM program, PFAM model, and computer server.--

On page 47, Table 1:

-- <u>Table 1:</u>

Accession #	E-value HMM	E-value HMM**	exo I	exo II	exo III
AAD25623 (SEQ ID NO:4)	4.6E-54	2.7E-67	D140, E142	D199	Y264, D268
AAC69936 (SEQ ID NO:6)	1.5E-44	5.8E-82	D80, E82	D138	Y203, D207
CAB36851 (SEQ ID NO:2)	2.0E-04	9.8E-12	D133, E135	D194	Y263, D267
AAC42241* (SEQ ID NO:22)	1.5E-01	<u>7.6E-27</u>	D50, E52	D108	A192, D196
AAD26968 SEQ ID NO:10)	5.1E+00	<u>=</u>	D61, Q63	D118	Q186, D190
AAC25931 (SEQ ID NO:12)	-	=	G70, Q72	D127	Q195, D199
AAF98185 (SEQ ID NO:14)	-	<u>:</u>	-	-?	Y60, R64
AAG50917 (SEQ ID NO:36)	-	<u>6.6E-11</u>	D384, E386	<u>D449</u>	Y531, D535
BAB11227 (SEQ ID NO:38)	-	2.4E-14	D34, E36	<u>D104</u>	Y186, D190
CAA80137 (SEQ ID NO:16)	-	<u>-</u>	D435, E437	D503	Y585, D589
AAF06162 (SEQ ID NO:18)	-	=	D82, E84	D143	Y212, D216

- *: using corrected sequence because 5' end is missing due to incorrect annotation, so that exo 1 may be present.
- **: HMM PFAM analysis done as per Method 3 of Example 1 exo I, II, & III motifs defined as in Figure 6 of Mian (1997) Nucleic Acids Res 25:3187--

On page 47-48, Table 2:

-- <u>Table 2:</u>

Accession #	E-value HMM	E-value HMM**	exo I	exo II	exo III
AAD25623 (SEQ ID NO:4)	4.6E-54	2.7E-67	136-145	191-206	261-271
AAC69936 (SEQ ID NO:6)	1.5E-44	5.8E-82	76-85	130-135	200-210
CAB36851 (SEQ ID NO:2)	2.0E-04	9.8E-12	129-138	186-201	260-270
AAC42241* (SEQ ID NO:22)	1.5E-01	7.6E-27	46-55	100-115	189-199
AAD26968 SEQ ID NO:10)	5.1E+00	<u> </u>	57-66	110-125	183-193
AAC25931 (SEQ ID NO:12)	-	Ξ	66-75	119-134	192-202
AAF98185 (SEQ ID NO:14)	-	Ξ	-	-	57-67
AAG50917 (SEQ ID NO:36)		6.6E-11	380-389	<u>441-456</u>	<u>528-538</u>
BAB11227 (SEQ ID NO:38)		2.4E-14	<u>30-39</u>	<u>96-111</u>	<u>183-193</u>
CAA80137 (SEQ ID NO:16)	-	-	431-440	495-510	582-592
AAF06162 (SEQ ID NO:18)	-	-	78-87	135-150	209-219

^{*:} using corrected sequence because 5' end is missing due to incorrect annotation, so that exo 1 may be present.

On page 53, third paragraph:

-- Alternatively, a nucleotide sequence set forth in any one of SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, [or] SEQ ID NO:17, SEQ ID NO:35 or SEQ ID NO:37 is included in a construct as described above and is used for overexpression of a polypeptide comprising a 3'-5' exonuclease domain.--

IN THE CLAIMS:

- 1. (amended) An isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain, and wherein said polypeptide is identical or substantially similar to an amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38.
- 4. (amended) An isolated nucleic acid molecule comprising a nucleotide sequence [=] identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21,

^{**:} HMM PFAM analysis done as per Method 3 of Example 1--

SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37.

- 12. (amended) An expression cassette comprising a nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain, and wherein said polypeptide is identical or substantially similar to an amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:16, SEQ ID NO:18,[or] SEQ ID No:24, SEQ ID NO:36 or SEQ ID NO:38, a promoter, and a terminator.
- 22. (amended) The plant cell according to claim 20, further comprising an endogenous nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37.
- 25. (amended) A plant cell comprising an endogenous nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, and wherein said plant cell comprises a mutation in said endogenous nucleotide sequence, or in a regulatory region thereof.
- 34. (amended) A plant cell capable of expressing a sense RNA molecule of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, and an anti-sense RNA molecule of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, wherein said sense and said anti-sense RNA molecules are capable of forming a double-stranded RNA molecule.
- 35. (amended) The plant cell according to claim 34, wherein the expression of the endogenous nucleotide sequence of said plant cell that is identical or substantially similar to SEQ

ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 is reduced.

- 44. (amended) A method for altering the expression in a plant cell or plant of an endogenous nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain, wherein said polypeptide is identical or substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38 comprising the step of: altering the transcription or translation of said endogenous nucleotide sequence in said plant cell or plant.
- 45. (amended) The method according to claim 44, wherein altering the transcription or translation of said endogenous nucleotide sequence in the plant cell or plant comprises the step of:
 - a) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1,SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 or a portion thereof, in sense orientation; or
 - b) expressing in said plant cell a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in anti-sense orientation; or
 - c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID
 - NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or
 - d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially

similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; or

- e) modifying by homologous recombination in said plant cell at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or of a regulatory region thereof; or f)expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or to a regulatory region thereof; or
- g) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a regulatory region thereof.
- 46. (amended) A method for altering the expression of an endogenous nucleotide sequence that is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37 in a plant cell or plant comprising the step of introducing into said plant cell a means for altering the transcription or translation of said endogenous nucleotide sequence in said plant cell.
- 47. (amended) A method for altering the expression of a nucleotide sequence of interest in a plant cell or plant comprising the steps of:
 - a) altering the expression in said plant cell or plant of an endogenous nucleotide sequence of said plant cell that is identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; and
 - b) introducing into said plant cell or plant a nucleic acid molecule comprising said nucleotide sequence of interest, wherein the expression of said nucleotide sequence of interest in said plant cell or plant is altered.

- 48. (amended) The method according to claim 47, wherein step a) comprises:
 - a) expressing in said plant cell or plant a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in sense orientation; or
 - b) expressing in said plant cell or plant a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, <u>SEQ ID NO:35 or SEQ ID NO:37</u>, or a portion thereof, in anti-sense orientation; or
 - c) expressing in said plant cell or plant a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ IDNO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9,SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or
 - d) expressing in said plant cell or plant a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37; or
 - e) modifying by homologous recombination in said plant cell or plant at least one chromosomal copy of the nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or of a regulatory region thereof; or

f)expressing in said plant cell or plant a zinc finger protein that is capable of binding to a nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, <u>SEQ ID NO:35 or SEQ ID NO:37</u>, or to a regulatory region thereof; or

- g) introducing into said plant cell or plant a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ IDNO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, <u>SEQ ID NO:35 or SEQ ID NO:37</u>, or a regulatory region thereof.
- 52. (amended)A method for stabilizing the expression of a nucleotide sequence of interest in a plant cell or plant comprising the steps of:
 - a) obtaining a plant cell or plant having altered expression in a plant cell of an endogenous nucleotide sequence of said plant cell or plant that encodes a polypeptide comprising a 3'-5' exonuclease domain, and wherein said polypeptide is identical or substantially similar to an amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38; and
 - b) introducing into said plant cell or plant a nucleotide sequence of interest, wherein the expression of said nucleotide sequence of interest in said plant cell is stabilized as compared to the expression of said nucleotide sequence of interest in a plant cell or plant lacking said first expression cassette.
- 53. (amended) The method according to claim 52, wherein said endogenous nucleotide sequence is identical or substantially similar to a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37.
- 54. (amended) The method according to claim 52, wherein the expression of said endogenous nucleotide sequence is altered by:
 - a) expressing in said plant cell a nucleotide sequence substantially similar to
 SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21,
 SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, [or]
 SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, in sense
 orientation; or
 - b) expressing in said plant cell a nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, <u>SEQ ID NO:35 or SEQ ID NO:37</u>, or a portion thereof, in anti-sense orientation; or

- c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, and an anti-sense RNA of said nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or
- d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, <u>SEQ ID NO:35 or SEQ ID NO:37</u>, or
- e) expressing in said plant cell an aptamer specifically directed to a polypeptide substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38, or
- f)modifying by homologous recombination in said plant cell at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or of a regulatory region thereof; or
- g) expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or to a regulatory region thereof; or
- h) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ IDNO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, [or] SEQ ID NO:23, SEQ ID NO:35 or SEQ ID NO:37, or a regulatory region thereof.
- 56. (amended) A method for identifying a compound capable of interacting with a polypeptide comprising a 3'-5' exonuclease domain comprising:

a) combining a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, [or] SEQ ID NO:24, SEQ ID NO:36 or SEQ ID NO:38, or a homolog thereof, and a compound to be tested for the ability to interact with said polypeptide, under conditions conducive to interaction; and b) selecting a compound from step (a) that is capable of interacting with said polypeptide.

IN THE SEQUENCE LISTING:

Please amend the sequence listing to add SEQ ID NOS; 35-38 as follows:

<210> 35
<211> 1749
<212> DNA
<213> Arabidopsis thaliana

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TACCTACTCA AAGAATGCTA TAAACATGGT AGCTTGAAGG CAACAAAAAA GTTCCAAGCT 180 TTACAGTATC AAGTTCATCG AGTTCTAGCT AATAAACCTC AACCAGGACC TGCTACTTTC 240 ATTATTAATT GTCTCACTTT ACTTCGTTTA TTTGGGGTAT ATGGTGAAGG CTTTAGTCAT 300 TTAGTTATAT CAGCTCTTCG CCGCTTCTTT AAAACAGTAT CTGAACCAAG CTTAGTCAAT 360 GATATTTGTT TGGGGAGAAA GCTAGCTGCT CAGTTCTTCC TTGACCCACT TAGTGAAGAA 360 GATATTGTT TGGGGAGAAA GCTAGCTGCT CAGTTCTTCC TTGACCCACT TAGTGAAGAA 360 GATATTGATT ATGGAGAAGG TATGGTGCT CAGTTCTTCC TTGCTACTGT TGGTGGATCT 420 TTAACTTATG ATGAGAAGGT TATGGTGCAT ACTCTTAGAG TGTTTGATGT GAGGTTAACT 480 AGTATCGATG AAGCCTTGTC TATCTCGGAA GTTTGGCAGA GATATGGGTT TGCTTGTGGA AATGCCTTCT TGGACAAATA CATTCTGAC TTGATCAAGT CGAAATCTTT CATGACGGCT 600 GTGACTCTGT TAGAGCAATT CTCTTTCCGT TTCCCTGGAG AAACTTTTTC TCAACAAATG 660 GTGACTCTGT TAGAGCAATT CTCTTTCCGT TTCCCTGGAG AAACTTTTCT TCAACAAATG 660 GTGACTCTGT TAGAGCAATT CTCTTTCCGT TCCCTGGAG AAACTTTTCT TCAACAAATG 660 GTGACTCTGT TTGTTCAAGA GTATGGCTCA AGGAATATGC TAAAGCAGGC CTATAAATATC 780 ATAAAAAAAAA ACTATCTACA GCATGACTTT CCCGAATTGT ATCACAAGTG TAAAGAAAGT 720 GTTGAGCACC TTCTGAAGA AAAAGCATGT TGGGATGTT ATCACAAAGTG TAAAGAAAGT 840 GCTCTGAAGG TTCTGCAGAA AAAAGCATGT TGGGATGTT CTGAAAAAAGT 900 GATAGACAGC TTCTGAAGTA TCTGGTATAC TTGGGATGTT CTGAAAAAAGT 960 GTTGATGAAC TCTGAAGATA TCTGGTATAC TTGGGATGTA AAGCACG AGAGGCTGAG 960 GTTGATTGT TTGAAAAAAAG CTTTCTGCGT CTCAACGATC TAGCTGAAA GATTGAGAAA GCTTGAAAAAAG CTTTCTGCGT CTCAACGATC TAGCTGAAA GATGTAGTT 1080 TGGGTTATG AAGTCAACGA GTTGAGAAAA GCAACTTCTT TTCTTGAAG AGAGGCTGAG 1020 GTGGCTTAGT AAGTCAACGA GTTGAGAAAA GCAACTTCTT TTCTTGAAGA AAATGTTT 1140 GTGGGTATG ACTGTGAAATC GACACCAC CTCAACGAC CTAGAAACCAC AAAAGGTT 1200 TCAATCATGC AAATTCGT CGGACACTGC CTCAACGAC TTTTGAAACAAA ATTTTCATAT TGGACTTGAT AAAGCACG AAACGGATACA 1320 TTAAAACACC CTGAAATTCT GGACAACTGC CTCAACAACTG TTTTGCAACC AAAACGGAA AAACCTAAT TATATTAAAG GCACTTGAT AAAGCACAC GACGAGGAACCAC CTAGACAACCAC CTCAACAACAC CTCAACAACAC CTCAACAACAC CTCAACAACAC TTTTGCAAC TTTTCAACAAAAAAAAAA	ATGGGTTTGG	ATTCTAAAGA	AGCTGATTTG	GAGGTAATAA	GAGATGAGAA	ATCTGAAGCA	60
TTACAGTATC AAGTTCATCG AGTTCTAGCT AATAAACCTC AACCAGGACC TGCTACTTTC 240 ATTATTAATT GTCTCACTTT ACTTCCTTTA TTTGGGGTAT ATGGTGAAGG CTTTAGTCAT 300 TTAGTTATAT CAGCTCTTCG CCGCTTCTTT AAAACAGTAT CTGAACCAAC TAGTGAAGAA 360 GATATTTGTT TGGCGAGAAA GCTAGCTGCT CAGTTCTTCC TTGCTACTGT TGGTGAATCA 420 TTAACTTATG ATGAGAAGGT TATGGTGCAT ACTCTTCC TTGCTACTGT TGGTGAACCA 480 AGTATCGATG AAGCCTTGTC TATCTCGGAA GTTTGGCAGA GATATGGGTT TGCTTGGATCT 420 AATGCGTTC TGGAACAATA CATTCTGAC TTGATCAGAG TGTTTGATGT GAGGTTAACT 480 AGTATCGATG AAGCCTTGTC TATCTCGGAA GTTTGGCAGA GATATGGGTT TGCTTGTGGA 540 AATGCGTTC TGGAACAATA CATTCTCGC TTGCCTGAGA GATATGGGTT TGCTTGTGGA 540 ATGACTCTGT TAGAGCATTT CTCTTTCCGT TCCCTGGAG GAAATCTTT CATGACGGCT 600 GTGACTCTGT TAGAGCATTT CTCTTTCCGT TCCCTGGAG AAACTTTTCT TCAACAAATG 660 GTGAGGATA AAAATTCCCA AGCTGCACAG AGATGGGCTA CCTCCATGGG AAGCCCAAGT 720 TTATGCATTC TTGTTCAAGA GTATGGCCTC AGGAATATGC TAAAAGCAAGC CTATAAATAC 780 ATAAATAAGA ACTATCTACA GCATGACCTA TCCCGGAATGC TAAAACAAGGT 740 GATAGACAGC TTCTGAAGAA TCTGGCATTC CCCGAATTGC TAAAACAAAGC 740 GATAGACAGC TTCTGAAGAA TCTGGTATAC TTGGCAGTGT ATCACAAGTG TAAAGAAAGT 960 GATAGACAGC TTCTGAAGTA TCTGGTATAC TTGGCAGTGT CCAAAAGCACG AGAGGCTGAG 1020 GTTGCTTTTG TTGAAAAAAG CTTTCTGCGT CTCAACGATC TAGCTGTAGA AGATTAGGTT 1080 GTGGGTTGATG AAGTCAACGA GTTGAGAAAAA GCAACTTCTT TCTTTGAAGG ATGTTAGGTT 1140 GTGGGTTGATG ACTGTGAATG GAAACCCAAA TTATTAAAGA GCAGTAAAAAGGT 1200 GTGGGTTATG ACTGTGAATG GAAACCCAAAA TTATTAAAGA GCAGTAAAAAGAT 1200 TCAATCATGC AAATTGGATC TGAAACCAAA ATTTTCAATAT TGGCAGTAA AAAGCATGT 1200 TCAATCATGC AAATTGGATC TGAAACCAAA ATTTTCAATAT TGGCAGTAA AAAGCATGT 1200 TTAAAGCCCT CTGAAATTCT GGACAACTGC CTTAGTCAA AATTACCCA AAATTGGATC TGAAACCAAA ATTTTCAATAT TGGCAGTAA AAACAAA GAACAAAGGTT 1200 TTAAAGCCCT CTGAAATTCT GGACAACTGC CTTAGTCAAA AATTATCACC AAATTGAAT 1380 TTTCAATCATG ACTCTCTGAC TGAGAACCTAT TATTAAAGC CCAGTAAAACAA GAACAAAGGTT 1200 TTAAAGCCCT TTGCAAAATTT TTTAATGAAC CATTTTGCAGA TTTCGAGGGA 1500 TTAAAGCCCT TTGCAAAATTTT TTAATGAAC CATTTGGAGT TTTAGCAGGA 1500 TTAAAGACAAA AAATTTGGG AGTGTCTTT AACAAAAAAAAA AATTTCCC AGGTTAAATTCA 1260 CAAAAGA	AACACTGTGT	GTTTACATGC	GTTTTCAGAT	TTAACCTATG	TGTCTCCTGT	TGTGTTCTTA	120
ATTATTAATT GTCTCACTTT ACTTCCTTTA TTTGGGGTAT ATGGTGAAGG CTTTAGTCAT TTAGTTATAT CAGCTCTTCG CCGCTTCTTT AAAACAGTAT CTGAACCAAC TAGTGAAGAA 360 GATATTTGTT TGGCGAGAAA GCTAGCTGCT CAGTTCTCC TTGCTACTGT TGGTGGATCT 420 TTAACTTATG ATGAGAAGGT TATGGTGCAT ACTCTTAGAG TGTTTGATGT GAGGTTAACT 480 AGTATCGATG AAGCCTTGTC TATCTCGGAA GTTTGGCAGA GATATGGGTT TGCTTGTGAA AATGCGTTTC TGGAACAATA CATTTCTGAC TTGATCAAGT GAGATATTTC CATGACGGCT 600 GTGACTCTGT TAGAGCATT CTCTTTCCGT TTCCCTGGAG AAACTTTTC TCAACAAATG 660 GTGACTCTGT TAGAGCATT CTCTTTCCGT TTCCCTGGAG AAACTTTCT TCAACAAATG 660 GTTGAGGATA AAAATTTCCA AGCTGCAGA GAGAGGCTA CCTTCATGGG AAGCCCAAGT 720 TTATGCATTC TTGTTCAAGA GTATGGCTCA AGGAATATGC TAAAGCAGGC CTATAATATC 780 ATAAATAAGA ACTATCTACA GCATGACTT CCGGAATTGT ATCACAAAGTG TAAAAAAAAGT 720 GATAGACAGC TTCTGAAGGA AAAAGCATGT TGGGGATTGT CTGAAATATAA GACAAAAAGGT 900 GATAGACAGC TTCTGAAGATA TCTGGTATAC TTGGCAGTGG AAGCTGGATA CTTGGAGAAG GTTGATGAAC TGTGCGAACA ATTCACATT CAGAGGGCTG CAAAAGCACG AGAGGCCAGG 960 GTTGATGAAC TGTGCGATCG ATATTCACTT CAAGGGCTGC CAAAAGCACG AGAGGCTGAG 1020 GTTGATGAAC TGTGCGATCG ATATTCACTT CAAGGGCTGC CAAAAGCACG AGAGGCTGAG 1020 GTTGATGAAC TGTGCGATCG ATATTCACTT CAAGGGCTGC CAAAAGCACG AGAGGCTGAG 1020 GTTGATGAAC AAATTGGAAC GTTGAGAAAAA GCAACTTCTT TTCTTGAAGA AGATTAAGTT 1080 GTGGGTATGT ACTGTGAATG GAAACCTAAT TATATTAAAA GCAAAAAGGT 1200 GTGACTCTTT CCTGAAGTA TATATTAAAAC CAATTGAACAA GAACAAGGTT 1200 TCAATCATGC AAATTGGATC TGATACCAAA ATTTTCATAT TGGACTAAC AAAAGCATC 1260 AATGACCGC TCTGAAATTCT GGACAACTAC TTTTCATAT TGGACTTGAT AAAGCTTTAC 1260 AATGACCGC TCTCTCTGAC TGATACCAAA ATTTTCATAT TGGACTTGAT AAAGCTTTAC 1260 AATGACGCCT CTGAAATTCT GGACAACTTAC TTATTCATAT TGGACTTGAT AAAGCTTTAC 1260 AATGACGCCT CTGAAATTCT TGAAACCAAA ATTTTCATATA GACAAAAACAA GAACAAAGGT 1320 TTAAAGCACG TCTCTCTGAC TGAAACCAAA ATTTTCATATA GACAAAAACAA GAACAAAGGT 1320 TTAAAGCACG TCTCTCTGAC TGAAACCAAA ATTTTTCATAT TGGACTTGAT AAAGCTTTAC 1260 AATGACGACT TGCAAAAATGTT TTTAATGGGG ATTTGAAAT TTTCAACAAGA AAATTTCAC 1260 CAAAAGCACT TGGCAGAA TCAACCTTTT TATATGAC CATTTGGTGG TTTTACAAGA 1500 CTAACGAAGA AAAATTTGGG AGTGCTCT TCAAAAA	TACCTACTCA	AAGAATGCTA	TAAACATGGT	AGCTTGAAGG	CAACAAAAA	GTTCCAAGCT	180
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TTTGAGGATA AAAATTTCCA AGCTGCAGAG AGATGGGCTA CCTTCATGGG AAGGCCAAGT 720 TTATGCATTC TTGTTCAAGA GTATGGCTCA AGGAATATGC TAAAGCAGGC CTATAATATC 780 ATAAATAAGA ACTATCTACA GCATGACTTT CCCGAATTGT ATCACAAGTG TAAAGAAAGT 840 GCTCTGAAGG TTCTGCAGAA AAAAGCATGT TGGGATGTTG CTGAAAATTAA GACAAAAGGT 900 GATAGACAGC TTCTGAAGTA TCTGGTATAC TTGGCAGTGG AAGCTGGATA CTTGGAGAAG 960 GTTGATGAAC TGTGCGATCG ATATTCACTT CAAGGGCTGC CAAAAGCACAG AGAGGCTGAG 1020 GTTGCTTTTG TTGAAAAAAG CTTTCTGCGT CTCAACGATC TAGCTGTAGA AGATGTAGTT 1080 TGGGTTGATG AAGTCAACGA GTTGAGAAAA GCAACTTCTT TTCTTGAAGG ATGTAGATT 1140 GTGGGTATTG ACTGTGAAT GAAACCTAAT TATATTAAAG GCAGTAAACA GAACAAGGTT 1200 TCAATCATGC AAATTGGATC TGATACCAAA ATTTTCATAT TGGACTTGAT AAAGCTTTAC 1260 AATGACGCCT CTGAAATTCT GGACAACTGC CTTAGTCACA TTTTGCAATC GAAGAGTACA 1320 TTAAAGCTCG TCTCTCTGAC TGAGGATTAC CCTGATCATA AATTATCCTC AGGTTACAAT 1380 TTTCAATGTG ACATCAAGCA GTTGGCGTT TCATATGGGG ATTTGAAAATG TTTCGAGGA 1440 TACGACATGT TGCTAGACAT TCAAAAATGTT TTTAATGAAC CATTTGGTGG TTTAGCAGGA 1500 CTAACGACAGA AAATATTGGG AGTGTCTTTG AACAAAACAA	AATGCGTTTC	TGGAACAATA	CATTTCTGAC	TTGATCAAGT	CGAAATCTTT	CATGACGGCT	600
TTATGCATTC TTGTTCAAGA GTATGGCTCA AGGAATATGC TAAAGCAGGC CTATAATATC 780 ATAAATAAGA ACTATCTACA GCATGACTTT CCCGAATTGT ATCACAAGTG TAAAGAAAGT 840 GCTCTGAAGG TTCTAGCAGA AAAAGCATGT TGGGATGTTG CTGAAATTAA GACAAAAGGT 900 GATAGACAGC TTCTGAAGTA TCTGGTATAC TTGGCAGTGG AAGCTGGATA CTTGGAGAAG 960 GTTGATGAAC TGTGCGATCG ATATTCACTT CAAGGGCTGC CAAAAGCACG AGAGGCTGAG 1020 GTTGCTTTTG TTGAAAAAAG CTTTCTGCGT CTCAACGATC TAGCTGTAGA AGATGTAGTT 1080 TGGGTTGATG AAGTCAACGA GTTCAGAAAA GCAACTTCTT TTCTTGAAGG ATGTAGAGTT 1140 GTGGGTATTG ACTGTGAATG GAAACCTAAT TATATTAAAG GCAGTAAACA GAACAAGGTT 1200 TCAATCATGC AAATTGGATC TGATACCAAA ATTTTCATAT TGGACTTGAT AAAGCTTTAC 1260 AATGACGCCT CTGAAATTCT GGACAACTGC CTTAGTCACA TTTTGCAAATC GAAGAGTACAA 1320 TTTAAAGCTCG TCTCTCTGAC TGAGGATTAC CCTGATCATA AATTATCCTC AGGTTACAAT 1380 TTTCAATGTG ACATCAAGCA GTTGGCGCTT TCATATGGGG ATTTGAAATG TTTCGAGCGA 1440 TACGACATGT TGCTAGACAT TCAAAATGTT TTTAATGAAC CATTTGGTG TTTAGCAGGA 1500 CTAACGAAGA AAATATTGGG AGTGTCTTTG AACAAAACAA	GTGACTCTGT	TAGAGCATTT	CTCTTTCCGT	TTCCCTGGAG	AAACTTTTCT	TCAACAAATG	660
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TGGGTTGATG AAGTCAACGA GTTGAGAAAA GCAACTTCTT TTCTTGAAGG ATGTAGAGTT 1140 GTGGGTATTG ACTGTGAATG GAAACCTAAT TATATTAAAG GCAGTAAACA GAACAAGGTT 1200 TCAATCATGC AAATTGGATC TGATACCAAA ATTTTCATAT TGGACTTGAT AAAGCTTTAC 1260 AATGACGCCT CTGAAATTCT GGACAACTGC CTTAGTCACA TTTTGCAATC GAAGAGTACA 1320 TTAAAGCTCG TCTCTCTGAC TGAGGATTAC CCTGATCATA AATTATCCTC AGGTTACAAT 1380 TTTCAATGTG ACATCAAGCA GTTGGCGCTT TCATATGGGG ATTTGAAATG TTTCGAGCGA 1440 TACGACATGT TGCTAGACAT TCAAAATGTT TTTAATGAAC CATTTGGTGG TTTAGCAGGA 1500 CTAACGAAGA AAATATTGGG AGTGTCTTTG AACAAAACAA	GTTGATGAAC	TGTGCGATCG	ATATTCACTT	CAAGGGCTGC	CAAAAGCACG	AGAGGCTGAG	1020
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Lys	Ser	Glu		Asn	Thr	Val	Cys	Leu 25	His	Ala	Phe	Ser	Asp	Leu	Thr
			20					25					30		
Tyr	Val		Pro	Val	Val	Phe			Leu	Leu	Lys		Cys	Tyr	Lys
-		35		-			40					45			
His	Gly	Ser	Leu	Lys	Ala	Thr	Lys	Lys	Phe	Gln	Ala	Leu	Gln	Tyr	Gln
	50					55		-			60				
Val	His	Arq	Val	Leu	Ala	Asn	Lys	Pro	Gln	Pro	Gly	Pro	Ala	Thr	Phe
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Tle	Tle	Asn	Cvs	I.e.i	Thr	Len	I.e.ii	Pro	T.em	Phe	Glv	Val	Tur	Glv	Glu
110			070	85	1111	Dea			90		<u> </u>		Tyr	95	
C1	Dho	C 0 15	uio	T 011	Wa 1	т1.	C 0 x	71-	T 011	7~~	7. ~~	Dho	Dho	T 110	Thr
GIA	Pne	Ser	100	Leu	val	тте	Ser	105	ьец	Arg	ALG	Pne	Phe 110	гуѕ	1111
									_						
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Ala		Gln	Phe	Phe	Leu			Val	Gly	Gly		Leu	Thr	Tyr	Asp
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1110	7114	Cys	180	71011			Dea	185					190		
T	C 0 20	T	Con	Dha	Mot	mb~	77.	17-1	Th w	T 011	T 011	C1.,	ui o	Dho	Co~
гуѕ	Ser	195	ser	Pile	мес	1111	200			Leu		205	His	rne	<u>ser</u>
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T.e.1	ጥህን	Hie	T.ve	Cvs	I.ve	Glii	Ser	Ala	T.e.11	Lve	Val	Ţ, e 11	Ala	Glu	Lvs
	_ + Y +	275	шys	- Cy3	دلات	<u> </u>	280	111.C	115 U	دور	· · · · ·	285	1114	Oru	11 7 3
	_		7		7.7		T 3	т.	m)	T .		7	70 .	G.3	т.
<u>Ala</u>	Cys	Trp	Asp	val	АТа	Glu	тте	Lys	Thr	ьуs	GLY	Asp	Arg	GIn	ьеu

	290					295					300				
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<u>Ile</u> 465	Lys	Gln	Leu	Ala	Leu 470	Ser	Tyr	Gly	Asp	Leu 475	Lys	Cys	Phe	Glu	Arg 480
Tyr	Asp	Met	Leu	Leu 485	Asp	Ile	Gln	Asn	Val 490	Phe	Asn	Glu	Pro	Phe 495	Gly
Gly	Leu	Ala	Gly 500			Lys	Lys		Leu	Gly	Val	Ser	Leu 510		Lys
Thr	Arg	Arg 515	Asn	Ser	Asp	Trp	Glu 520	Gln	Arg	Pro	Leu	Ser 525	Gln	Asn	Gln
Leu	Glu 530	Tyr	Ala	Ala	Leu	Asp 535	Ala	Ala	Val	Leu	Ile 540	His	Ile	Phe	Arg
His 545	Val	Arg	Asp	His	Pro 550	Pro	His	Asp	Ser	Ser 555	Ser	Glu	Thr	Thr	Gln 560
Trp	Lys	Ser	His	Ile 565	Val	Ser	Thr	Ser	Tyr 570	Lys	Ser	Pro	Tyr	Leu 575	Ser
Ser	Asp	Asn	Ser 580	Arg	Arg										

<210> 37 <211> 1518 <212> DNA <213> Arabidopsis thaliana

ATGGAGACCA ATCTAAAGAT CTATCTAGTT TCATCCACCG ACTCGTCCGA GTTCACTCAC 60 CTGAAATGGT CTTTCACCTG TTCTACGATC ATCGCCTTAG ACGCCGAATG GAAGCCACAA 120 CACTCCAATA CGTCGTCGTT TCCGACCGT ACCCCTCCC AAGTCGCAGT CAGCCCACAGT 180 CACGCCACGG ATGTCTCCGA TGTCTCCCT ATTGATTTGA GTCGCATTCA TCTCCATCG 240 GTTTGGGAGC TGTTGAATGA TATGTTCGTG TCGCCGGATG GTTCGATCA TCTTCCATCG 240 GTTTGGGAGC TGTTGAATGA TATGTTCGTG TCGCCGGATG TTCTGAAACT AGGGTTTCGG 300 TTTCAAACAGG ATTTGGTTTA CTTGTCTTCG ACATTTACTC AACATGGATG TGAAGGTGGA 360 TTCCAAGAGG TGAAACAATA CTTGGATATT ACAAGCATAT ACAATTATCT GCAACATAAG 420 CGGTTTGGGA GAAAGCCCC AAAGGATATC AAGAGCTTGG CTGCTATATC TAAGAGAAATG 480 CTGGACATCT CTCTCTCAAA GGAACTCAA TGTAGTGTT GGTCAATATC TAAGAGAAATG 480 CTGGACATCT CTCTCTCAAA GGAACTCAA TGTAGTGATT GGTCAATATCG TCCTCTTACA 540 GAAGAACAGA AACTATACGC TGCCACAGAT GCTCACTGC TGCTCCAGAT ATTCGATGTA 600 TTTGAGGCGC ATCTTGTTGA AGGAATCACA GTGCAAGATC TTAGGAGTGA TATCGATGTAT 600 TTTGAGAGCAA TCTTGTTGA ATCGACCTAA AGCACTAAGA TTTGATTGGC 660 TTACAAGAAA TCTTGATCA ATCGACCTAA AGCACTAAGA TTGTCACAGT CAAACCTTTGC 720 AAGGCTACAG ATGTAATCAG ATCAATGTCG GAAAATGGTC AAAACATAGC CAATGGATG 780 GTTCCAAGAA AACGACACT AACACCGATC CCAATGGATC TTCTACCAAA GAAACTTTGC 740 AAGGAACTTTG GAGAACCGAT CCTGTTGAAC GAGTTTGTT TAGGCGGTGA TGTCTCTTACA AACACCGATC CCAATGGATC TTCTACCAAA GAAACTTTAGG 900 AAGAAAACAA GAAGACGTC CCCCTCAAGC ACTATGAAC CAAATAAGCA GTTGGTCTGT 960 TCTGCGGGACT GGCAAGGTC CCCCTCAAGC ACTATGAACA CAAATAAGCA GTTGGTCTGT 960 AAGAAAACAA GAAGACGTT CCCCCTCAAGC ACTATGAACA CACAATAAGCA GTTGGTCTGT 960 AAGACAACAA TCCCACACCT AAACACGAAT TTGAGGTGAT TTCTACCAAA GAAACTTTAAG 900 AAGACAACAA TCCCACACCT AAAGAGAGT TTGAAGGA TTCTACGATG TTGAGGATTTC TAAGGAATT 1080 GATGCTGCAA TCCCACACCT AAAGAGAGT TCCCAAGGA ATCTACTTT TAGGCGGTGA TGTGGTCTGT 1020 AAATTTCTAT TGGATGTGAT GGTTGAAGGT TTGCAAGGA TTCAAGGA TTCAAGGA TTCCACACCACCA GGATTTCGCA TCCCACACCAC AAAAAAATAGC AAAAAATAGC AAAAAATTGC AAAGAGAAT TCCACACACCA CAAAAAAATAGC CAAATAAGCA GAGTTCTTC TAAAGAAGAT ACAAAAATTGT TGAAGGAATT TGAAGGAATT TGAAGGAATT TAACAAAAAATTATT TTGAAGCAAC TCCAACACCA CAAAAAAATAGC AAAAAATAGC AAAAAAATAGC AA							
CTGAAATGGT CTTTCACTCG TTCTACGATC ATCGCCTTAG ACGCCGAATG GAAGCCACAA 120 CACTCCAATA CGTCGTCGTT TCCGACCGTC ACTCTCCTC AAGTCGCATG CCGACTCAGT 180 CACGCCACGG ATGTCTCCGA TGTCTTCCTC ATTGATTTGA GTTCGATTCA TCTTCCATCG 240 GTTTGGGAGC TGTTGAATGA TATGTTCGTG TCGCCGGATG TTCTGAAACT AGGGTTTCGG 300 TTTAAACAGG ATTTGGTTTA CTTGGATTAT ACAAGCATAT ACAATTATCT CAACATGGATG TGAAACATAG 360 TTCCAAGAGG TGAAACAATA CTTGGATTAT ACAAGCATAT ACAATTATCT GCAACATAAG 420 CGGTTTGGGA GAAACAATA CTTGGATTAT ACAAGCATAT ACAATTATCT CAACATAAG 480 CTGGACATCT CTCTCTCAAA GGAACTTCAA TGTACTGGT CTCCTCTTACA 540 GAAGAACAGA AACTATACGC TGCCACAGAT GCTCACTGCC TGCTCCAGAT ATTCGATGTA 660 TTTGAGGGCG ATCTTGTTGA AGGAATCACA GTGCAAGATC TAGAGGTGAT AAATTTGCC 660 TTACAAGAAA TTCTGACTGA ATCGGACTAT AGCACTAAGA TTTCTCACAGT CAAACTTTGC 720 AAGGCTACAG ATGTAATCAG ATCAATTCTCG GAAAATGGTC AAAACACTAGC CAAACTTTGC 720 AAGGCTACAG ATGTAATCAG ATCAATTCTCG GAAAATGGTC AAAACACTAGC CAATGGATG 780 GTTCCAAGAA AAACGACCAT AAACACGAAT CCCAATGGATG AGAATTTGT GAAGATTTGC 840 AGGAAGTTTG GAGAACGGAT CCTGTTGAAG GAGATTGAAC CAAATTAGC CAATGGATG 780 AAGAAAACAA GAAACGCGAT CCTGTTCAAG GAGATTGAACA CAAATTAGC CAATGGATG 900 AAGAAAACAA GAAGACGTC ACCGCCATGG GACTCTCTT TAGGCGGTGA TGGCTCGCT 1020 AAATTTCTAT TGGATGTGAT GGTTGAAGG ACTATCAACA CAAATAAGCA GTTGGTCTGT 960 TCTGCGGACT GGCAAGGTC CCCCCTCAAGC ACTATCATCT TAGGCGGTGA TGGCTCCCT 1020 AAATTTCTAT TGGATGTGAT GGTTGAAGG TTGGCGAACAC ATCTACGTTG TGTGGGGATT 1080 GATGCTGCAA TCCCACACTC AAAGAAGAGT TTGGCGAAAC ATCTACGTTG TGTGGGGATT 1080 GATGCTGCAA TCCCACACTC AAAGAAGAC ACACTATCTT TAGGCGGTGA TCAAGCATTC 1140 AAAGAGAACA GAGTTCTATT AACAAGAAGT ACAAAATTGT TGAGACACCA GGATTTGGCA 1200 AAGCATCAAA TATATCGAGT AAAGAGAGT CCTTAAAGAG ACTGATGTT TGAGACACCA GGATTTGGCA 1200 AAGCATCAAA TATATCGAGT AAAGAGAGT CCAGCGATTT TCAAAGAAC CAAATTAGGC AAAGAGTTC TTGAGGGAATT TCAAGAGAT CAGCGGAAATT TCAAAGAACC CAAAGAGATC CAGCGGAAAT CAGCGGAAAT TATATCGAGT AAAGAGAGT CCAGCGGAAT TCAAGAGAT CAGCGGAAAT TATATCGAGT AAAACACGAT TCAAACACGA CAGCACT TAGAGCACC AAAGGGTTC TAAAGAGAT CAGCGGAAAT TATAACAAA AATTTAAACAAA AATTTAAACAAA AATTTAAACAAA AATTTAAACAAA AATTTAAAC	<400> 37						
CACTCCAATA CGTCGTCGTT TCCGACCGTC ACTCTCCTC AAGTCGCATG CCGACTCAGT 180 CACGCCACGG ATGTCTCCGA TGTCTTCCTC ATTGATTTGA GTTCGATTCA TCTTCCATCG 240 GTTTGGGAGC TGTTGAATGA TATGTTCGTG TCGCCGGATG TTCTGAAACT AGGGTTTCGG 300 TTTAAACAGG ATTTGGTTTA CTTGTCTTCG ACATTTACTC AACATGGATG TGAAGGTGGA 360 TTCCAAGAGG TGAAACAATA CTTGGATATT ACAAGCATAT ACAATTATCT GCAACATAAG 420 CGGTTTGGGA GAAAGGCGC AAAGGATAT ACAAGCATAT GCAACATAAG 480 CTGGACATCT CTCTCTCAAA GGAACTTCAA TGTAGTGATT GGTCCATATG TAAGGAATG 480 CTGGACATCT CTCTCTCAAA GGAACTTCAA TGTAGTGATT GGTCCATATG TCCCTCTTACA 540 GAAGAACAGA AACTATACGC TGCCACAGAT GCTCACTGCC TGCTCCAGAT ATTCGATGTA 660 TTTGAGGCGC ATCTTGTTGA AGGAATCACA GTGCAAGATC TTAGGATGAT AAATGTTGGC 660 TTACAAGAAA TTCTGACTGA ATCGGACTAT AGCAATAGAC TTAGGATGAT AAATGTTGGC 720 AAGGCTACAG ATGTAATCAG ATCAATGTC GAAAATTGGTC AAAACATTAGC CAATGGATG 780 GTTCCAAGAA AAACGACACT AAACACGATG CCAATGGATG AGAATTTGTT GAAGATTGTC 720 AAGGAACACA AGAACGGAT CCTGTTGAAG GAGCTTGATC TCCTCAAA GAAACTTTGC 780 GTTCCAAGAA AAACGACACT AAACACGATG CCAATGGATG AGAATTTGTT GAAGATTGTC 840 AGGAAGTTTG GAGAACGGAT CCTGTTGAAG GAGTCTGATC TTCTACCAAA GAAACTTTAG 900 AAGAAAACAA GAAGACGGAT CCTGTTGAAG ACTATGAACA CAAATAAGCA GTTGGTCTGT 960 CTGCGGGACT GGCAAGGTC CCCCCAAGG GACTCATCTT TAGGCGGTGA TGGCTGCCCT 1020 AAATTTCTAT TGGATGTGAT GGTTGAAGGT TTGGCGAAAC ATCTACGTTG TGTGGGGATT 1080 GATGCTGCAA TCCCACACCC AAAGAAGGGT TTGGGGAAAC ATCTACGTTG TGTGGGGATT 1080 GATGCTGCAA TCCCACACCC AAAGAAGGGT TCTAAAAGGA ACTACACT TGAGGACCA GGATTTGGCC 1140 AAAGAGAACA GAGTTCTATT AACAAGAGAT ACAAAATTGT TGAGACACCA GGATTTGGCC 1200 AAACTTCCAACATC AAAGAAGCC GATTCAAAGGA ACTACACTAC	ATGGAGACCA	ATCTAAAGAT	CTATCTAGTT	TCATCCACCG	ACTCGTCCGA	GTTCACTCAC	60
CACGCCACGG ATGTCTCCGA TGTCTTCCTC ATTGATTTGA GTTCGATTCA TCTTCCATCG 240 GTTTGGGAGC TGTTGAATGA TATGTTCGTG TCGCCGGATG TTCTGAAACT AGGGTTTCGG 300 TTTAAACAGG ATTTGGTTTA CTTGTCTTCG ACATTTACTC AACATGGATG TGAAGGTGGA 360 TTCCAAGAGG TGAAACAATA CTTGGATATT ACAAGCATAT ACAATTATCT GCAACATAAG 420 CGGTTTGGGA GAAAGGCGC AAAGGATATC AAGAGCTTGG CTGCTATATG TAAGGAAATG 480 CTGGACATCT CTCTCTCAAA GGAACTTCAA TGTAGTGATT GGTCATATG TCCTCTTACA 540 GAAGACACAGA AACTATACGC TGCCACAGAT GCTCACTGCC TGCTCCAGAT ATTCGATGTA 600 TTTGAGGCGC ATCTTGTTGA AGGAATCACA GTGCAAGATC TTAGAGGATA AAATGTTGGC 660 TTACAAGAAA TTCTGACTGA ATCGGACTAT AGCAGTAGA TTGGTCACAGT CAAACCTTTGC 720 AAGGCTACAG ATGTAATCAG ATCAATGTCG GAAAATGGTC AAAACATAGC CAAAGCTTGC 780 GTTCCAAGAA AAACGACACT AAACACGATG CCAATGGATG AGAATTTGTT GAAGATTGTC 780 GTTCCAAGAA AAACGACACT AAACACGATG CCAATGGATG AGAATTTGTT GAAGATTGTC 840 AGGAAGTTTG GAGAACGGAT CCTGTTGAAG GAGTCTGATC TTCTACCAAA GAAACTTTAG 900 AAGAAAACAA GAAGACGGAT CCTGTTGAAG GAGTCTGATC TTCTACCAAA GAAACTTAAG 900 AAGAAAACAA GAAGACGGAT CCGCCCATGG GACTCATCTT TAGGCGGTGA TGGCTGCCCT 1020 AAATTTCTAT TGGATGTGAT GGTTGAAGGT TTGGCGAAAC ATCTACGATG TGGCTGCCT 1020 AAATTTCTAT TGGATGTGAT GGTTGAAGGT TTGGCGAAAC ATCTACGTTG TGGGGGATT 1080 GATGCTGCAA TCCCACACTC AAAGAAGCCG GACTCATCTT TAGGCGGTGA TGCTGCCCT 1020 AAATTTCTAT TGGATGTGAT GGTTGAAGGT TTGGCGAAAC ATCTACGTTG TCAAGCATTC 1140 AAAGGAAACA GAGTTCTATT AACAAGAAGCC GATTCAAGG AGTTGCTTGA TCAAGCATTC 1140 AAAGAGAACA GAGTTCTATT AACAAGAAGGT CCTTAAAAGG AGTTCCTTGA TCAAGCATTC 1140 AAAGGAACA TATATCGAGT AAAGAAGCC GAATATGT TGAGACACCA GGATTTGGCA 1200 AAGCATCAAA TATATCGAGT AAAGAAGCCT CTTAAAAATG ACAAAATTGT TGAGACACCA GGATTTGGCA 1200 AAGCATCAAA TATATCGAGT AAAGAAGCTT CTTAAAAATG ACAAAATTGT TGAGACACCA GGATTTGGCA 1200 GAGACTTTCC AGCCGAAAC CTCTAAGCAT CAAAAATTGT TGAGACACCA GGATTTGGCA 1200 GAGACTTTCC AGCGGAAAC CTCTAAGCAT CAAAAATTGT TGAGACACCA GGATTTGGCA 1200 GAGACTTTCC AGCGGAAAC CTCTAAGCAT CAAAAATTGT TGAGACACCA GAAGTTCC 1380 CAAAGAATAC CCAACTGCTT ATTTAACAAA AATTTAGAGT TTTGGCAAGT CATGAACTGC 1440 CATCAACTAT ACTGGGAGGG AACTCAGTAT CATAACGCAG TCCAGAAGTT CATGAA	CTGAAATGGT	CTTTCACTCG	TTCTACGATC	ATCGCCTTAG	ACGCCGAATG	GAAGCCACAA	120
GTTTGGGAGC TGTTGAATGA TATGTTCGTG TCGCCGGATG TTCTGAAACT AGGGTTTCGG 300 TTTAAACAGG ATTTGGTTTA CTTGTCTTCG ACATTTACTC AACATGGATG TGAAGGTGGA 360 TTCCAAGAGG TGAAACAATA CTTGGATATT ACAAGCATAT ACAATTATCT GCAACATAAG 420 CGGTTTGGGA GAAAGGCGCC AAAGGATATC AAGAGCTTGG CTGCTATATG TAAGGAAATG 480 CTGGACATCT CTCTCTCAAA GGAACTTCAA TGTAGTGATT GGTCATATCG TCCTCTTACA 540 GAAGACAGA AACTATACGC TGCCACAGAT GCTCACTGCC TGCTCCAGAT ATTCGATGTA 600 TTTGAGGCGC ATCTTGTTGA AGGAACTCAA GTGCAAGATC TTAGAGTGAT AAATGTTGGC 660 TTACAAGAAA TTCTGACTGA ATCGGACTAT AGCAAGATC TTAGAGTGAT AAATGTTGGC 720 AAGGCTACAG ATGTAATCAG ATCAATGTCG GAAAATGGTC AAAACATAGC CAAACTTTGC 780 GTTCCAAGAA AAACGACACT AAACACGATG CCAATGGATG AGAATTTGTT GAAGATTGTC 840 AGGAAGTTTG GAGAACGGAT CCTGTTGAAG GAGTCTGATC TTCTACCAAA GAAACTTAAG 900 AAGAAAACAA GAAGACGGAT CCTGTTGAAG GAGTCTGATC TTCTACCAAA GAAACTTAAG 900 AAGAAAACAA GAAGACGGTC CGCCCCAAGG ACTATGAACA CAAATAAGCA GTTGGTCTGT 960 TCTGCGGGACT GGCAAGGTC ACCGCCATGG GACTCATCTT TAGGCGGTGA TGGCTGCCCT 1020 AAATTTCTAT TGGATGTGAT GGTTGAAGGT TTGGCGAAAC ATCTACGTTG TGTGGGGATT 1080 GATGCTGCAA TCCCACACTC AAAGAAGCCG GATTCAAGGG AGTTGCTTGA TCAAGCATTC 1140 AAAGAGAAACA GAGTTCTATT AACAAGAAGCC GATTCAAGGG AGTTGCTTGA TCAAGCATTC 1140 AAAGAGAACA GAGTTCTATT AACAAGAAGAT ACAAAATTGT TGAAGCACCA GGATTTGGCC 1200 AAAGAACAAA TATATCGAGT AACAAGATCT CTTAAAAATG AGCAGCTACT TGAGGTGATA 1260 GAGACTTCC AGCTAAAGAT CAGCGGAAT CCACAGTGT CCAGATGTAC GAGATGTAC TGAGGTGATA 1260 GAGACTTCCA ACCTCAAAGAT CAGCGGAAT CCACAGTGT CCAGATGTAC TGAGGTGATA 1260 GAGACTTTCC AGCTAAAGAT CAGCGGAAT CCAGATGTAC TGAGGTGATA 1260 GAGACTTTCC AGCTAAAGAT CAGCGGAAT CAGCAGTGT TTGAGACACCA GAATTGGCA 1200 AAGGAATTAC CCACACTC AAAGAAGCTT TAAAAAGATTG TGAGACACCA GAATTGGCA 1200 AAGGATCAAA TATATCGAGT AAAGAGGTTT CTTAAAAATG AGCAGCTACT TGAGGTGATA 1260 GAGACTTTCC AGCTAAAAGAT CAGCGGAAT TAGAAGAGCTA TTGAAGCAGC AAAGGGTTTC 1380 CAAAAGAATAC CCAACTGCTT ATTTAACAAA AATTTAGAGT TTTGGCAAGT CATGAACTGC 1440 CAACACTATA ACTGGGAGGG AACTCAGTAT CATAACGCAG TCCAGAAGTT CATGAACTGC 1440	CACTCCAATA	CGTCGTCGTT	TCCGACCGTC	ACTCTCCTCC	AAGTCGCATG	CCGACTCAGT	180
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TTCCAAGAGG TGAAACAATA CTTGGATATT ACAAGCATAT ACAATTATCT GCAACATAAG 420 CGGTTTGGGA GAAAGGCGCC AAAGGATATC AAGAGCTTGG CTGCTATATG TAAGGAAATG 480 CTGGACATCT CTCTCTCAAA GGAACTTCAA TGTAGTGATT GGTCATATCG TCCTCTTACA 540 GAAGAACAGA AACTATACGC TGCCACAGAT GCTCACTGCC TGCTCAGAT ATTCGATGTA 600 TTTGAGGCGC ATCTTGTTGA AGGAATCACA GTGCAAGATC TTAGAGTGAT AAATGTTGGC 660 TTACAAGAAA TTCTGACTGA ATCGACTAT AGCAGTAAGA TTGTCACAGT CAAACTTTGC 720 AAGGCTACCAG ATGTAATCAG ATCAATGTCG GAAAATGGTC AAAACATAGC CAATGGAGTG 780 GTTCCAAGAA AAACGACACT AAACACGATG CCAATGGATG AGAATTTGTT GAAGATTGTC 840 AGGAAGTTTG GAGAACGGAT CCTGTTGAAG GAGTCTGATC TTCTACCAAA GAAACTTAAG 900 AAGAAAACAA GAAGACGGAT CCTGTTGAAG GAGTCTGATC TTCTACCAAA GAAACTTAAG 900 AAGAAAACAA GAAGACGGAT CGCCCCAAGG ACTATGAACA CAAATAAGCA GTTGGTCTGT 960 TCTGCGGACT GGCAAGGTC ACCGCCATGG GACTCATCTT TAGGCGGTGA TGGCTGCCCT 1020 AAATTTCTAT TGGATGTGAT GGTTGAAGGT TTGGCGAAAC ATCTACGTTG TGTGGGGATT 1080 GATGCTGCAA TCCCACACCC AAAGAAGCCG GATTCAAGGG AGTTGGTCTGT TGAGACACCA GGATTTGGC 1140 AAAGAGAACA GAGTTCTATT AACAAGAAGGT ACAAAATTGT TGAGACACCA GGATTTGGCA 1200 AAGCATCAAA TATATCGAGT AAAGAGCCG GATTCAAGGG AGTTGCTAC TGAGGCTATC 1140 AAAGAGAACA TATATCGAGT AAAGAGCCG GATTCAAGGG AGCACTACT TGAGGCGATA 1260 AAGCATCAAA TATATCGAGT AAAGAGATCT CTTAAAAATG ACCAGCTACT TGAGGTGATA 1260 GAGACATTTC AGCTAAAGAT CAGCGGAAT CAGCAGTGT CCAGATGTAC GAAGTGCCAT 1320 GAGACATTTC AGCTAAAGAT CAGCGGAAT CAGCAGTGT CCAGATGTAC GAAGTGCCAT 1380 CAAAGAATAC CCAACTGCTT ATTTAACAAA AATTTAGAGT TTTGGCAAGTG CATGAACTGC 1440 CAACAACTAT ACTGGGAGGG AACTCAGTAT CATAACGCAG TCCAGAAGTT CATGGAAGTT 1360 CAAAGAATAC CCAACTGCTT ATTTAACAAA AATTTAGAGT TTTGGCAAGTT CATGAACTGC 1440 CATCAACTAT ACTGGGAGGG AACTCAGTAT CATAACGCAG TCCAGAAGTT CATGGAAGTA 1500	GTTTGGGAGC	TGTTGAATGA	TATGTTCGTG	TCGCCGGATG	TTCTGAAACT	AGGGTTTCGG	300
CGGTTTGGGA GAAAGGCGCC AAAGGATATC AAGAGCTTGG CTGCTATATG TAAGGAAATG CTGGACATCT CTCTCTCAAA GGAACTTCAA TGTAGTGATT GGTCATATCG TCCTCTTACA 540 GAAGAACAGA AACTATACGC TGCCACAGAT GCTCACTGCC TGCTCCAGAT ATTCGATGTA 600 TTTGAGGGCG ATCTTGTTGA AGGAATCACA GTGCAAGATC TTAGAGTGAT AAATGTTGGC 660 TTACAAGAAA TTCTGACTGA ATCGGACTAT AGCAGTAAGA TTGTCACAGT CAAACTTTGC 720 AAGGCTACCA ATGTAATCAG ATCAGTCG GAAAATGGTC AAAACATAGC CAATGGAGTG 780 GTTCCAAGAA AAACGACACT AAACACGATG CCAATGGATG AGAATTTGTT GAAGATTGTC 840 AGGAAGTTTG GAGAACGGAT CCTGTTGAAG GAGTTGATC TTCTACCAAA GAAACTTAAG 900 AAGAAAACAA GAAGACGTG CGCCTCAAGC ACTATGAACA CAAATAAGCA GTTGGTCTGT 960 TCTGCGGACT GGCAAGGTC ACCGCCATGG GACTCATCTT TAGGCGGTGA TGGCTGCCT 1020 AAATTTCTAT TGGATGTGAT GGTTGAAGGT TTGGCGAAC ATCTACGTTG TGTGGGGATT 1080 GATGCTGCAA TCCCACACC AAAGAAGCC GATTCAAGGG AGTTGGTCTGT 140 AAAGAGAACA GAGTTCTATT AACAAGAGGT CTTAAAGGA AGCACTACT TGAGGCATC 1200 AAGCATCAAA TATATCGAGT AAAGAGCC GATTCAAGGG AGCACTACT TGAGGCATC 1200 AAGCATCAAA TATATCGAGT AAAGAAGCTT CTTAAAAATG AGCAGCTACT TGAGGTGATA 1200 AGGAAATTTC AGCTAAAGAT CAGCGGAAT CAGCAGTGT CCAGAATTAC GAAGTGCCA 1200 CAAAGAATAC CACACTC AAAGAACCT CTTAAAAATG AGCAGCTACT TGAGGTGATA 1260 GGGAAATTTC AGCTAAAGAT CAGCGGAAT CAGCAGTGT CCAGAAGTT CAGGAGTTT 1320 GGGAAATTTA TCCAGAAACC TCTAAACAA AATTTAGAGT TTGAAACCAG AAAGGGTTTC 1380 CAAAGAATAC CCAACTGCTT ATTTAACAAA AATTTAGAGT TTTGGCAAGTG CATGAACTGC 1440 CAACACTAT ACTGGGAGGG AACTCAGTAT CATAACGCAG TCCAGAAGTT CATGGAAGTA 1500	TTTAAACAGG	ATTTGGTTTA	CTTGTCTTCG	ACATTTACTC	AACATGGATG	TGAAGGTGGA	360
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CATCAACTAT ACTGGGAGGG AACTCAGTAT CATAACGCAG TCCAGAAGTT CATGGAAGTA 1500	GGGAAATTTA	TTCAGAAACC	TCTAAGCATT	GAAGAAGCTA	TTGAAGCAGC	AAAGGGTTTC	1380
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			20					25					30		
Leu	Asp	Ala	Glu	Trp	Lys	Pro	Gln	His	Ser	Asn	Thr	Ser	Ser	Phe	Pro
		35					40					45			
,															
Thr	Val	Thr	Leu	Leu	Gln	Val	Ala	Cys	Arg	Leu	Ser	His	Ala	Thr	Asp
	50					55					60				
Val	Ser	Asp	Val	Phe	Leu	Ile	Asp	Leu	Ser	Ser	Ile	His	Leu	Pro	Ser
65					70					75					80
Val	Trp	Glu	Leu	Leu	Asn	Asp	Met	Phe	Val	Ser	Pro	Asp	Val	Leu	Lys
				85					90				,	95	
Leu	Gly	Phe	Arg	Phe	Lys	Gln	Asp	Leu	Val	Tyr	Leu	Ser	Ser	Thr	Phe
			100					105					110		

Thr	Gln	His 115	Gly	Cys	Glu	Gly	Gly 120	Phe	Gln	Glu	Val	Lys 125	Gln	Tyr	Leu
Asp	Ile 130	Thr	Ser	Ile	Tyr	Asn 135	Tyr	Leu	Gln	His	Lys 140	Arg	Phe	Gly	Arg
Lys 145	Ala	Pro	Lys	Asp	Ile 150	Lys	Ser	Leu	Ala	Ala 155	Ile	Cys	Lys	Glu	<u>Met</u> 160
Leu	Asp	Ile	Ser	Leu 165	Ser	Lys	Glu	Leu	Gln 170	Cys	Ser	Asp	Trp	Ser 175	Tyr
Arg	Pro	Leu	Thr 180	Glu	Glu	Gln	Lys	Leu 185	Tyr	Ala	Ala	Thr	Asp 190	Ala	His
Cys	Leu	Leu 195	Gln	Ile	Phe	Asp	Val 200	Phe	Glu	Ala	His	Leu 205	Val	Glu	Gly
<u>Ile</u>	Thr 210	Val	Gln	Asp	Leu	Arg 215	Val	Ile	Asn	Val	Gly 220	Leu	Gln	Glu	Ile
Leu 225	Thr	Glu	Ser	Asp	Tyr 230	Ser	Ser	Lys	Ile	Val 235	Thr	Val	Lys	Leu	Cys 240
Lys	Ala	Thr	Asp	Val 245	Ile	Arg	Ser	Met	Ser 250	Glu	Asn	Gly	Gln	Asn 255	Ile
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Asp	Glu	Asn 275	Leu	Leu	Lys	Ile	Val 280	Arg	Lys	Phe	Gly	Glu 285	Arg	Ile	Leu
Leu	Lys 290	Glu	Ser	Asp	Leu	Leu 295	Pro	Lys	Lys	Leu	Lys 300	Lys	Lys	Thr	Arg
Arg 305	Arg	Val	Ala	Ser	Ser 310	Thr	Met	Asn	Thr	Asn 315	Lys	Gln	Leu	Val	Cys 320
Ser	Ala	Asp	Trp	Gln 325	Gly	Pro	Pro	Pro	Trp 330	Asp	Ser	Ser	Leu	Gly 335	Gly
Asp	Gly	Cys	Pro 340	Lys	Phe	Leu	Leu	Asp 345	Val	Met	Val	Glu	Gly 350	Leu	Ala
Lys	His	Leu 355	Arg	Cys	Val	Gly	Ile 360	Asp	Ala	Ala	Ile	Pro 365	His	Ser	Lys
Lys	Pro 370	Asp	Ser	Arg	Glu	Leu 375	Leu	Asp	Gln	Ala	Phe 380	Lys	Glu	Asn	Arg
<u>Val</u> 385	Leu	Leu	Thr	Arg	Asp 390	Thr	Lys	Leu	Leu	Arg 395	His	Gln	Asp	Leu	Ala 400
Lys	His	Gln	Ile	Tyr 405	Arg	Val	Lys	Ser	Leu 410	Leu	Lys	Asn	Glu	Gln 415	Leu

Leu	Glu	Val	Ile	Glu	Thr	Phe	Gln	Leu	Lys	Ile	Ser	Gly	Asn	Gln	Leu
			420					425					430		
Met	Ser		Cys	Thr	Lys	Cys		Gly	Lys	Phe	Ile		Lys	Pro	Leu
		435					440					445			
Ser		Glu	Glu	Ala	Ile		Ala	Ala	Lys	Gly		Gln	Arg	Ile	Pro
	450		,			455					460				
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403					370					475					- 100
His	Gln	Leu	Tyr	Trp 485	Glu	Gly	Thr	Gln	Tyr 490	His	Asn	Ala	Val	Gln 495	Lys
<u>Phe</u>	Met	Glu	Val 500	Cys	Lys	Leu	Ser	Glu 505							